

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals S.A.

&lt;120&gt; Novel compounds

&lt;130&gt; BM45353

&lt;160&gt; 4

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 1239

&lt;212&gt; DNA

&lt;213&gt; Neisseria meningitidis

&lt;400&gt; 1

atggctttttt atgcttttaa ggcgatgcgt gcggccgcgt tggctgccgc cgttgcatcg	60
gtactgtcgt cttgcggtaa aggcggagac gcggcgagg gcgggcagcc tgctggtcgg	120
gaagcccctg cggcgcgtcg cgggtgtcgta accgtccatc cgcaaaccgt cgcattgacc	180
gtcgaagtgc cggggcgctt ggaatcgctg cgtaccgccg atgtccgcgc ccaagtcggc	240
ggcatcatcc aaaaacgcct gttccaagaa ggcagttatg tccgtgccgg acagccgctg	300
tatcagatcg acagttccac ttatgaagca aatctggaaa gcgcgcgcgc gcaactggca	360
acggctcagg caacgcctgc caaagcggat gcggatttgg cgcgatacaa gcctttgggt	420
gccgccgaag ccgtcagccg gcaggaatac gatgctgcgg taacggcgaa acgttctgcc	480
gaggcagggtg tcaaagcagc acaggcggca atcaaactcg ccggcattaa tctgaaccgt	540
tcgcgcatta ccgcgccgat ttccggcttt atcggtcagt ccaaagtctc cgaaggtag	600
ctgttgaaatg cgggcgatac gaccgtgctg gcaaccatcc gccaaaccaa tccgatgtat	660
gtgaacgtta ccagtcctgc atccgaagtg atgaaattgc gccgtcagat agccgaaggc	720
aaactgctgg cggcggtatg tgtgattgcg gtcggcatca aatttgacga cggcacagtt	780
taccctgaaa aaggccgcct gctgtttgcc gatccggctg tcaacgaatc gaccggtcag	840
attaccctgc gcgccgccgt accgaacgat cagaatatcc tgatgcccg tctgtatgtg	900
cgcggtgctga tggaccaagt ggcgggtggat aacgcatttg ttgtgccgca gcaggcggta	960
acgcgcgggtg cgaaagatac cgtgatgatt gtgaatgcc aaggcgggtat ggaacccgc	1020
gaggtaacgg ttgcgcaaca gcagggtacg aattggattg ttacgtcggg tctgaaggac	1080
ggggacaagg tggttgtgga aggcacagt atcgccggtg taacgggtgc gaaaaaggta	1140
acgcccgaag aatgggcgtc gtctgaaaac caagccgcgc gcctcaatc cggcgttcag	1200

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acggcatctg aagccaaaac tgcttctgaa gcggaataa

1239

&lt;210&gt; 2

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Neisseria meningitidis

&lt;400&gt; 2

Met Ala Phe Tyr Ala Phe Lys Ala Met Arg Ala Ala Ala Leu Ala Ala  
 1 5 10 15  
 Ala Val Ala Leu Val Leu Ser Ser Cys Gly Lys Gly Gly Asp Ala Ala  
 20 25 30  
 Gln Gly Gly Gln Pro Ala Gly Arg Glu Ala Pro Ala Pro Val Val Gly  
 35 40 45  
 Val Val Thr Val His Pro Gln Thr Val Ala Leu Thr Val Glu Leu Pro  
 50 55 60  
 Gly Arg Leu Glu Ser Leu Arg Thr Ala Asp Val Arg Ala Gln Val Gly  
 65 70 75 80  
 Gly Ile Ile Gln Lys Arg Leu Phe Gln Glu Gly Ser Tyr Val Arg Ala  
 85 90 95  
 Gly Gln Pro Leu Tyr Gln Ile Asp Ser Ser Thr Tyr Glu Ala Asn Leu  
 100 105 110  
 Glu Ser Ala Arg Ala Gln Leu Ala Thr Ala Gln Ala Thr Leu Ala Lys  
 115 120 125  
 Ala Asp Ala Asp Leu Ala Arg Tyr Lys Pro Leu Val Ala Ala Glu Ala  
 130 135 140  
 Val Ser Arg Gln Glu Tyr Asp Ala Ala Val Thr Ala Lys Arg Ser Ala  
 145 150 155 160  
 Glu Ala Gly Val Lys Ala Ala Gln Ala Ala Ile Lys Ser Ala Gly Ile  
 165 170 175  
 Asn Leu Asn Arg Ser Arg Ile Thr Ala Pro Ile Ser Gly Phe Ile Gly  
 180 185 190  
 Gln Ser Lys Val Ser Glu Gly Thr Leu Leu Asn Ala Gly Asp Thr Thr  
 195 200 205  
 Val Leu Ala Thr Ile Arg Gln Thr Asn Pro Met Tyr Val Asn Val Thr  
 210 215 220  
 Gln Ser Ala Ser Glu Val Met Lys Leu Arg Arg Gln Ile Ala Glu Gly  
 225 230 235 240  
 Lys Leu Leu Ala Ala Asp Gly Val Ile Ala Val Gly Ile Lys Phe Asp  
 245 250 255

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Asp Gly Thr Val Tyr Pro Glu Lys Gly Arg Leu Leu Phe Ala Asp Pro  
                   260                                  265                                  270  
 Val Val Asn Glu Ser Thr Gly Gln Ile Thr Leu Arg Ala Ala Val Pro  
                   275                                  280                                  285  
 Asn Asp Gln Asn Ile Leu Met Pro Gly Leu Tyr Val Arg Val Leu Met  
                   290                                  295                                  300  
 Asp Gln Val Ala Val Asp Asn Ala Phe Val Val Pro Gln Gln Ala Val  
 305                                  310                                  315                                  320  
 Thr Arg Gly Ala Lys Asp Thr Val Met Ile Val Asn Ala Gln Gly Gly  
                                   325                                  330                                  335  
 Met Glu Pro Arg Glu Val Thr Val Ala Gln Gln Gln Gly Thr Asn Trp  
                   340                                  345                                  350  
 Ile Val Thr Ser Gly Leu Lys Asp Gly Asp Lys Val Val Val Glu Gly  
                   355                                  360                                  365  
 Ile Ser Ile Ala Gly Ile Thr Gly Ala Lys Lys Val Thr Pro Lys Glu  
                   370                                  375                                  380  
 Trp Ala Ser Ser Glu Asn Gln Ala Ala Ala Pro Gln Ser Gly Val Gln  
 385                                  390                                  395                                  400  
 Thr Ala Ser Glu Ala Lys Thr Ala Ser Glu Ala Glu  
                                   405                                  410

&lt;210&gt; 3

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 3

aggcagaggc atatggcttt ttatgctttt aaggcgatgc g

41

&lt;210&gt; 4

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer

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PCT/EP00/00425

&lt;400&gt; 4

aggcagagggc tcgagttccg cttcagaagc agttttggct tc

42